<110> ITOH, Kyogo
SHICHIJO, Shigeki
IMAI, Yasuhisa

<120> TUMOR ANTIGEN PROTEINS, GENES THEREFOR, AND TUMOR ANTIGEN PEPTIDES

<130> 0020-4491P

<140> 09/202,047
<141> 1998-12-07

<160> 2

<170> PatentIn Ver. 2.1

<210> 1
<211> 2527
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(2527)
<223> Strandedness: Double-stranded

<220>
<221> 5'UTR
<222> (1)..(38)

E1

<220>
<221> CDS
<222> (39)..(2438)

<220>
<221> 3'UTR
<222> (2439)..(2506)

<220>
<221> polyA_site
<222> (2507)..(2527)

<400> 1
```
ggttcggcgg cagccgggct cggagtggac gtgccact atg ggg tcg tcc aag aag 56
                                          Met Gly Ser Ser Lys Lys
                                            1               5
cat cgc gga gag aag gag gcg gcc ggg acg acg gcg gcg gcc ggc acc  104
His Arg Gly Glu Lys Glu Ala Ala Gly Thr Thr Ala Ala Ala Gly Thr
            10                  15                  20
ggg ggt gcc acc gag cag ccg ccg cgg cac cgg gaa cac aaa aaa cac  152
Gly Gly Ala Thr Glu Gln Pro Pro Arg His Arg Glu His Lys Lys His
        25                  30                  35
aag cac cgg agt ggc ggc agt ggc ggt agc ggt ggc gaa cga cgg aag  200
Lys His Arg Ser Gly Gly Ser Gly Gly Ser Gly Gly Glu Arg Arg Lys
    40                  45                  50
cgg agc cgg gaa cgt ggg ggc gag cgc ggg agc ggg cgg cgc ggg gcc  248
Arg Ser Arg Glu Arg Gly Gly Glu Arg Gly Ser Gly Arg Arg Gly Ala
55                  60                  65                  70
```

```
gaa gct gag gcc cgg agc agc acg cac ggg cgg gag cgc agc cag gca   296
Glu Ala Glu Ala Arg Ser Ser Thr His Gly Arg Glu Arg Ser Gln Ala
                75                  80                  85
gag ccc tcc gag cgg cgc gtg aag cgg gag aag cgc gat gac ggc tac   344
Glu Pro Ser Glu Arg Arg Val Lys Arg Glu Lys Arg Asp Asp Gly Tyr
            90                  95                  100
gag gcc gct gcc agc tcc aaa act agc tca ggc gat gcc tcc tca ctc   392
Glu Ala Ala Ala Ser Ser Lys Thr Ser Ser Gly Asp Ala Ser Ser Leu
        105                 110                 115
agc atc gag gag act aac aaa ctc cgg gca aag ttg ggg ctg aaa ccc   440
Ser Ile Glu Glu Thr Asn Lys Leu Arg Ala Lys Leu Gly Leu Lys Pro
    120                 125                 130
ttg gag gtt aat gcc atc aag aag gag gcg ggc acc aag gag gag ccc   488
Leu Glu Val Asn Ala Ile Lys Lys Glu Ala Gly Thr Lys Glu Glu Pro
135                 140                 145                 150
gtg aca gct gat gtc atc aac cct atg gcc ttg cga cag cga gag gag   536
Val Thr Ala Asp Val Ile Asn Pro Met Ala Leu Arg Gln Arg Glu Glu
                155                 160                 165
ctg cgg gag aag ctg gcg gct gcc aag gag aag cgc ctg ctg aac caa   584
Leu Arg Glu Lys Leu Ala Ala Ala Lys Glu Lys Arg Leu Leu Asn Gln
            170                 175                 180
aag ctg ggg aag ata aag acc cta gga gag gat gac ccc tgg ctg gac   632
Lys Leu Gly Lys Ile Lys Thr Leu Gly Glu Asp Asp Pro Trp Leu Asp
        185                 190                 195
gac act gca gcc tgg atc gag agg agc cgg cag ctg cag aag gag aag   680
Asp Thr Ala Ala Trp Ile Glu Arg Ser Arg Gln Leu Gln Lys Glu Lys
    200                 205                 210
gac ctg gca gag aag agg gcc aag tta ctg gag gag atg gac caa gag   728
Asp Leu Ala Glu Lys Arg Ala Lys Leu Leu Glu Glu Met Asp Gln Glu
215                 220                 225                 230
ttt ggt gtc agc act ctg gtg gag gag gag ttc ggg cag agg cgg cag   776
Phe Gly Val Ser Thr Leu Val Glu Glu Glu Phe Gly Gln Arg Arg Gln
                235                 240                 245
gac ctg tac agt gcc cgg gac ctg cag ggc ctc acc gtg gag cat gcc   824
Asp Leu Tyr Ser Ala Arg Asp Leu Gln Gly Leu Thr Val Glu His Ala
            250                 255                 260
att gat tcc ttc cga gaa ggg gag aca atg att ctt acc ctc aag gac   872
Ile Asp Ser Phe Arg Glu Gly Glu Thr Met Ile Leu Thr Leu Lys Asp
        265                 270                 275
aaa ggc gtg ctg cag gag gag gag gac gtg ctg gtg aac gtg aac ctg   920
Lys Gly Val Leu Gln Glu Glu Glu Asp Val Leu Val Asn Val Asn Leu
    280                 285                 290
gtg gat aag gag cgg gca gag aaa aat gtg gag ctg cgg aag aag aag   968
Val Asp Lys Glu Arg Ala Glu Lys Asn Val Glu Leu Arg Lys Lys Lys
295                 300                 305                 310
cct gac tac ctg ccc tat gcc gag gac gag agc gtg gac gac ctg gcg  1016
Pro Asp Tyr Leu Pro Tyr Ala Glu Asp Glu Ser Val Asp Asp Leu Ala
                315                 320                 325
cag caa aaa cct cgc tct atc ctg tcc aag tat gac gaa gag ctt gaa  1064
Gln Gln Lys Pro Arg Ser Ile Leu Ser Lys Tyr Asp Glu Glu Leu Glu
            330                 335                 340
ggg gag cgg cca cat tcc ttc cgc ttg gag cag ggc ggc acg gct gat  1112
Gly Glu Arg Pro His Ser Phe Arg Leu Glu Gln Gly Gly Thr Ala Asp
        345                 350                 355
ggc ctg cgg gag cgg gag ctg gag gag atc cgg gcc aag ctg cgg ctg  1160
Gly Leu Arg Glu Arg Glu Leu Glu Glu Ile Arg Ala Lys Leu Arg Leu
    360                 365                 370
cag gct cag tcc ctg agc aca gtg ggg ccc cgg ctg gcc tcc gaa tac  1208
Gln Ala Gln Ser Leu Ser Thr Val Gly Pro Arg Leu Ala Ser Glu Tyr
375                 380                 385                 390
```

E1 cont

```
ctc acg cct gag gag atg gtg acc ttt aaa aag acc aag cgg agg gtg   1256
Leu Thr Pro Glu Glu Met Val Thr Phe Lys Lys Thr Lys Arg Arg Val
                395                 400                 405
aag aaa atc cgc aag aag gag aag gag gta gta gtg cgg gca gat gac   1304
Lys Lys Ile Arg Lys Lys Glu Lys Glu Val Val Val Arg Ala Asp Asp
            410                 415                 420
ttg ctg cct ctc ggg gac cag act cag gat ggg gac ttt ggt tcc aga   1352
Leu Leu Pro Leu Gly Asp Gln Thr Gln Asp Gly Asp Phe Gly Ser Arg
        425                 430                 435
ctg cgg gga cgg ggt cgc cgc cga gtg tcc gaa gtg gag gag gag aag   1400
Leu Arg Gly Arg Gly Arg Arg Arg Val Ser Glu Val Glu Glu Glu Lys
    440                 445                 450
gag cct gtg cct cag ccc ctg ccg tcg gac gac acc cga gtg gag aac   1448
Glu Pro Val Pro Gln Pro Leu Pro Ser Asp Asp Thr Arg Val Glu Asn
455                 460                 465                 470
atg gac atc agt gat gag gag gaa ggt gga gct cca ccg ccg ggg tcc   1496
Met Asp Ile Ser Asp Glu Glu Glu Gly Gly Ala Pro Pro Pro Gly Ser
                475                 480                 485
ccg cag gtg ctg gag gag gac gag gcg gag ctg gag ctg cag aag cag   1544
Pro Gln Val Leu Glu Glu Asp Glu Ala Glu Leu Glu Leu Gln Lys Gln
            490                 495                 500
ctg gag aag gga cgc cgg ctg cga cag tta cag cag cta cag cag ctg   1592
Leu Glu Lys Gly Arg Arg Leu Arg Gln Leu Gln Gln Leu Gln Gln Leu
        505                 510                 515
cga gac agt ggc gag aag gtg gtg gag att gtg aag aag ctg gag tct   1640
Arg Asp Ser Gly Glu Lys Val Val Glu Ile Val Lys Lys Leu Glu Ser
    520                 525                 530
cgc cag cgg ggc tgg gag gag gat gag gat ccc gag cgg aag ggg gcc   1688
Arg Gln Arg Gly Trp Glu Glu Asp Glu Asp Pro Glu Arg Lys Gly Ala
535                 540                 545                 550
atc gtg ttc aac gcc acg tcc gag ttc tgc cgc acc ttg ggg gag atc   1736
Ile Val Phe Asn Ala Thr Ser Glu Phe Cys Arg Thr Leu Gly Glu Ile
                555                 560                 565
ccc acc tac ggg ctg gct ggc aat cgc gag gag cag gag gag ctc atg   1784
Pro Thr Tyr Gly Leu Ala Gly Asn Arg Glu Glu Gln Glu Glu Leu Met
            570                 575                 580
gac ttt gaa cgg gat gag gag cgc tca gcc aac ggt ggc tcc gaa tct   1832
Asp Phe Glu Arg Asp Glu Glu Arg Ser Ala Asn Gly Gly Ser Glu Ser
        585                 590                 595
gac ggg gag gag aac atc ggc tgg agc acg gtg aac ctg gac gag gag   1880
Asp Gly Glu Glu Asn Ile Gly Trp Ser Thr Val Asn Leu Asp Glu Glu
    600                 605                 610
aag cag cag cag gat ttc tct gct tcc tcc acc acc atc ctg gac gag   1928
Lys Gln Gln Gln Asp Phe Ser Ala Ser Ser Thr Thr Ile Leu Asp Glu
615                 620                 625                 630
gaa ccg atc gtg aat agg ggg ctg gca gct gcc ctg ctc ctg tgt cag   1976
Glu Pro Ile Val Asn Arg Gly Leu Ala Ala Ala Leu Leu Leu Cys Gln
                635                 640                 645
aac aaa ggg ctg ctg gag acc aca gtg cag aag gtg gcc cgg gtg aag   2024
Asn Lys Gly Leu Leu Glu Thr Thr Val Gln Lys Val Ala Arg Val Lys
            650                 655                 660
gcc ccc aac aag tcg ctg ccc tca gcc gtg tac tgc atc gag gat aag   2072
Ala Pro Asn Lys Ser Leu Pro Ser Ala Val Tyr Cys Ile Glu Asp Lys
        665                 670                 675
atg gcc atc gat gac aag tac agc cgg agg gag gaa tac cga ggc ttc   2120
Met Ala Ile Asp Asp Lys Tyr Ser Arg Arg Glu Glu Tyr Arg Gly Phe
    680                 685                 690
aca cag gac ttc aag gag aag gac ggc tac aaa ccc gac gtt aag atc   2168
Thr Gln Asp Phe Lys Glu Lys Asp Gly Tyr Lys Pro Asp Val Lys Ile
695                 700                 705                 710
```

E1 Cont

```
gaa tac gtg gat gag acg ggc cgg aaa ctc aca ccc aag gag gct ttc   2216
Glu Tyr Val Asp Glu Thr Gly Arg Lys Leu Thr Pro Lys Glu Ala Phe
                715                 720                 725
cgg cag ctg tcg cac cgc ttc cat ggc aag ggc tca ggc aag atg aag   2264
Arg Gln Leu Ser His Arg Phe His Gly Lys Gly Ser Gly Lys Met Lys
            730                 735                 740
aca gag cgg cgg atg aag aag ctg gac gag gag gcg ctc ctg aag aag   2312
Thr Glu Arg Arg Met Lys Lys Leu Asp Glu Glu Ala Leu Leu Lys Lys
        745                 750                 755
atg agc tcc agc gac acg ccc ctg ggc acc gtg gcc ctg ctc cag gag   2360
Met Ser Ser Ser Asp Thr Pro Leu Gly Thr Val Ala Leu Leu Gln Glu
    760                 765                 770
aag cag aag gct cag aag acc ccc tac atc gtg ctc agc ggc agc ggc   2408
Lys Gln Lys Ala Gln Lys Thr Pro Tyr Ile Val Leu Ser Gly Ser Gly
775                 780                 785                 790
aag agc atg aac gcg aac acc atc acc aag tgacagcgcc ctcccgtagt     2458
Lys Ser Met Asn Ala Asn Thr Ile Thr Lys
                795                 800
cggccctgcc tcaaccttca tattaaataa agctccctcc ttatttttaa aaaaaaaaaa 2518
aaaaaaaaa                                                         2527
```

<210> 2
<211> 800
<212> PRT
<213> Homo sapiens

<400> 2

```
Met Gly Ser Ser Lys Lys His Arg Gly Glu Lys Glu Ala Ala Gly Thr
  1               5                  10                  15
Thr Ala Ala Ala Gly Thr Gly Gly Ala Thr Glu Gln Pro Pro Arg His
             20                  25                  30
Arg Glu His Lys Lys His Lys His Arg Ser Gly Gly Ser Gly Gly Ser
         35                  40                  45
Gly Gly Glu Arg Arg Lys Arg Ser Arg Glu Arg Gly Gly Glu Arg Gly
     50                  55                  60
Ser Gly Arg Arg Gly Ala Glu Ala Glu Ala Arg Ser Ser Thr His Gly
 65                  70                  75                  80
Arg Glu Arg Ser Gln Ala Glu Pro Ser Glu Arg Arg Val Lys Arg Glu
                 85                  90                  95
Lys Arg Asp Asp Gly Tyr Glu Ala Ala Ala Ser Ser Lys Thr Ser Ser
            100                 105                 110
Gly Asp Ala Ser Ser Leu Ser Ile Glu Glu Thr Asn Lys Leu Arg Ala
        115                 120                 125
Lys Leu Gly Leu Lys Pro Leu Glu Val Asn Ala Ile Lys Lys Glu Ala
    130                 135                 140
Gly Thr Lys Glu Glu Pro Val Thr Ala Asp Val Ile Asn Pro Met Ala
145                 150                 155                 160
Leu Arg Gln Arg Glu Glu Leu Arg Glu Lys Leu Ala Ala Ala Lys Glu
                165                 170                 175
Lys Arg Leu Leu Asn Gln Lys Leu Gly Lys Ile Lys Thr Leu Gly Glu
            180                 185                 190
Asp Asp Pro Trp Leu Asp Asp Thr Ala Ala Trp Ile Glu Arg Ser Arg
        195                 200                 205
Gln Leu Gln Lys Glu Lys Asp Leu Ala Glu Lys Arg Ala Lys Leu Leu
    210                 215                 220
Glu Glu Met Asp Gln Glu Phe Gly Val Ser Thr Leu Val Glu Glu Glu
225                 230                 235                 240
Phe Gly Gln Arg Arg Gln Asp Leu Tyr Ser Ala Arg Asp Leu Gln Gly
                245                 250                 255
```

Leu Thr Val Glu His Ala Ile Asp Ser Phe Arg Glu Gly Glu Thr Met
260 265 270
Ile Leu Thr Leu Lys Asp Lys Gly Val Leu Gln Glu Glu Glu Asp Val
275 280 285
Leu Val Asn Val Asn Leu Val Asp Lys Glu Arg Ala Glu Lys Asn Val
290 295 300
Glu Leu Arg Lys Lys Lys Pro Asp Tyr Leu Pro Tyr Ala Glu Asp Glu
305 310 315 320
Ser Val Asp Asp Leu Ala Gln Gln Lys Pro Arg Ser Ile Leu Ser Lys
325 330 335
Tyr Asp Glu Glu Leu Glu Gly Glu Arg Pro His Ser Phe Arg Leu Glu
340 345 350
Gln Gly Gly Thr Ala Asp Gly Leu Arg Glu Arg Glu Leu Glu Glu Ile
355 360 365
Arg Ala Lys Leu Arg Leu Gln Ala Gln Ser Leu Ser Thr Val Gly Pro
370 375 380
Arg Leu Ala Ser Glu Tyr Leu Thr Pro Glu Glu Met Val Thr Phe Lys
385 390 395 400
Lys Thr Lys Arg Arg Val Lys Lys Ile Arg Lys Lys Glu Lys Glu Val
405 410 415
Val Val Arg Ala Asp Asp Leu Leu Pro Leu Gly Asp Gln Thr Gln Asp
420 425 430
Gly Asp Phe Gly Ser Arg Leu Arg Gly Arg Gly Arg Arg Arg Val Ser
435 440 445
Glu Val Glu Glu Glu Lys Glu Pro Val Pro Gln Pro Leu Pro Ser Asp
450 455 460
Asp Thr Arg Val Glu Asn Met Asp Ile Ser Asp Glu Glu Glu Gly Gly
465 470 475 480
Ala Pro Pro Pro Gly Ser Pro Gln Val Leu Glu Glu Asp Glu Ala Glu
485 490 495
Leu Glu Leu Gln Lys Gln Leu Glu Lys Gly Arg Arg Leu Arg Gln Leu
500 505 510
Gln Gln Leu Gln Gln Leu Arg Asp Ser Gly Glu Lys Val Val Glu Ile
515 520 525
Val Lys Lys Leu Glu Ser Arg Gln Arg Gly Trp Glu Glu Asp Glu Asp
530 535 540
Pro Glu Arg Lys Gly Ala Ile Val Phe Asn Ala Thr Ser Glu Phe Cys
545 550 555 560
Arg Thr Leu Gly Glu Ile Pro Thr Tyr Gly Leu Ala Gly Asn Arg Glu
565 570 575
Glu Gln Glu Glu Leu Met Asp Phe Glu Arg Asp Glu Glu Arg Ser Ala
580 585 590
Asn Gly Gly Ser Glu Ser Asp Gly Glu Glu Asn Ile Gly Trp Ser Thr
595 600 605
Val Asn Leu Asp Glu Glu Lys Gln Gln Gln Asp Phe Ser Ala Ser Ser
610 615 620
Thr Thr Ile Leu Asp Glu Glu Pro Ile Val Asn Arg Gly Leu Ala Ala
625 630 635 640
Ala Leu Leu Leu Cys Gln Asn Lys Gly Leu Leu Glu Thr Thr Val Gln
645 650 655
Lys Val Ala Arg Val Lys Ala Pro Asn Lys Ser Leu Pro Ser Ala Val
660 665 670
Tyr Cys Ile Glu Asp Lys Met Ala Ile Asp Asp Lys Tyr Ser Arg Arg
675 680 685
Glu Glu Tyr Arg Gly Phe Thr Gln Asp Phe Lys Glu Lys Asp Gly Tyr
690 695 700
Lys Pro Asp Val Lys Ile Glu Tyr Val Asp Glu Thr Gly Arg Lys Leu
705 710 715 720
Thr Pro Lys Glu Ala Phe Arg Gln Leu Ser His Arg Phe His Gly Lys
725 730 735

Gly Ser Gly Lys Met Lys Thr Glu Arg Arg Met Lys Lys Leu Asp Glu
740 745 750

Glu Ala Leu Leu Lys Lys Met Ser Ser Ser Asp Thr Pro Leu Gly Thr
755 760 765

Val Ala Leu Leu Gln Glu Lys Gln Lys Ala Gln Lys Thr Pro Tyr Ile
770 775 780

Val Leu Ser Gly Ser Gly Lys Ser Met Asn Ala Asn Thr Ile Thr Lys
785 790 795 800